

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2005, 06:03:39 ; Search time 3394 Seconds  
(Without alignments)  
10964.527 Million cell updates/sec

Title: US-09-939-537-32  
Perfect score: 768  
Sequence: 1 GCTAGAGAGAGCCCAATCTT.....GGGCTGTGACGACGATCC 768

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenBank:1:  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_cm:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_srs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	768	100.0	768	6	AR067945 Sequence
2	768	100.0	768	6	AR166804 Sequence
3	768	100.0	768	6	AR560090 Sequence
4	744.6	97.0	3134	9	BC019046 Homo sapi
5	738.2	96.1	3075	6	CQ851090 Sequence
6	738.2	96.1	3075	9	AK128301 Homo sapi
7	701	91.3	3183	6	CQ851340 Sequence
8	701	91.3	3183	9	AK128579 Homo sapi
9	701	91.3	4240	9	AK090464 Homo sapi
10	695.2	90.5	7427	6	CQ768745 Sequence
11	695.2	90.5	7493	6	CQ768742 Sequence
12	694.4	90.4	1413	6	AX556949 Sequence
13	694.4	90.4	1413	6	AX709548 Sequence
14	694.4	90.4	1428	6	AR031186 Sequence
15	694.4	90.4	1428	6	AR042591 Sequence
16	694.4	90.4	1428	6	AR052284 Sequence
17	694.4	90.4	1428	6	AR076262 Sequence
18	694.4	90.4	1428	6	AR300619 Sequence
19	694.4	90.4	1431	6	AR108863 Sequence

20	694.4	90.4	1431	6	AR108867 Sequence
21	694.4	90.4	1431	6	AR265197 Sequence
22	694.4	90.4	1431	6	AR265201 Sequence
23	694.4	90.4	1431	6	AR488219 Sequence
24	694.4	90.4	1431	6	AR488223 Sequence
25	694.4	90.4	1431	6	BD063035 Identific
26	694.4	90.4	1431	6	BD063039 Identific
27	694.4	90.4	1437	6	AR108865 Sequence
28	694.4	90.4	1437	6	AR265199 Sequence
29	694.4	90.4	1437	6	AR488221 Sequence
30	694.4	90.4	1437	6	BD063037 Identific
31	694.4	90.4	8540	6	BD004713 Chimeric
32	694.4	90.4	9209	6	AR000007 Sequence
33	694.4	90.4	9209	6	AR015961 Sequence
34	694.4	90.4	9209	6	AR060920 Sequence
35	694.4	90.4	9209	6	AR211052 Sequence
36	694.4	90.4	9209	6	AR454341 Sequence
37	694.4	90.4	9209	6	AX032414 Sequence
38	694.4	90.4	9209	6	BD004714 Chimeric
39	694.4	90.4	18986	6	AR051652 Sequence
40	694.4	90.4	18986	6	AR092290 Sequence
41	694.4	90.4	18986	6	BD075126 Method fo
42	693.8	90.3	1367	6	AX039182 Sequence
43	693.6	90.3	1173	6	AX392220 Sequence
44	693.6	90.3	1173	6	AX818092 Sequence
45	693.4	90.3	1528	12	AF272772 Synthetic

#### ALIGNMENTS

RESULT 1  
AR067945  
LOCUS AR067945 768 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 32 from patent US 5851828.  
ACCESSION AR067945  
VERSION AR067945.1 GI:5999167  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 768)  
AUTHORS Seed,B., Banapour,B., Romeo,C. and Kolanus,W.  
TITLE Targeted cytolysis of HIV-infected cells by chimeric CD4  
receptor-bearing cells  
JOURNAL Patent: US 5851828-A 32 22-DEC-1998;  
FEATURES  
source Location/Qualifiers  
1..768  
/organism="unknown"  
/mol\_type="unassigned DNA"

#### ORIGIN

Query Match 100.0%; Score 768; DB 6; Length 768;  
Best Local Similarity 100.0%; Pred. No. 1.1e-139;  
Matches 768; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTAGAGAGCCCAATCTTGTGACAAACTACACATGCCCGCCAGACACTGA 60  
DB 1 GCTAGAGAGCCCAATCTTGTGACAAACTACACATGCCCGCCAGACACTGA 60  
QY 1 ACTCCTGGGGGAGCCTCAGTCTTCTTCTTCCCAAAACCAAGACACCTCATGAT 120  
DB 1 ACTCCTGGGGGAGCCTCAGTCTTCTTCTTCCCAAAACCAAGACACCTCATGAT 120  
QY 121 CTCCTGGACCCCTGAGGTCAATGCTGTGTGTGACGTGAGCCAGAAAGCCTTGAAGT 180  
DB 121 CTCCTGGACCCCTGAGGTCAATGCTGTGTGTGACGTGAGCCAGAAAGCCTTGAAGT 180  
QY 121 CTTCCGACCCCTGAGGTCAATGCTGTGTGTGACGTGAGCCAGAAAGCCTTGAAGT 240  
DB 121 CTTCCGACCCCTGAGGTCAATGCTGTGTGTGACGTGAGCCAGAAAGCCTTGAAGT 240  
QY 181 CAACTTCACTGTATGTGACGCGCTGTGAGGATTAATGCCAAGACGCGGGGA 240  
DB 181 CAACTTCACTGTATGTGACGCGCTGTGAGGATTAATGCCAAGACGCGGGGA 240  
QY 241 GGAGCAGTACACAGCAGTACCGGGTGTGACGCTCTTCAACCGCTTGCACGAGACTG 300

Db 241 GGAGCGTACCAAGACGTCACGGGTGTGAGGCTCTCTCAACCGTCTGCAAGACTG 300  
QY 301 GGTGATGGCAAGAGTACAGTGAAGTCTCCAAACAAGCCCTCCAGCCCCCATGCA 360  
Db 301 GGTGATGGCAAGAGTACAGTGAAGTCTCCAAACAAGCCCTCCAGCCCCCATGCA 360  
QY 361 GAAAAACAATCTCCAAAGCCAAAGGGGAGCCCGGAGAAACAAGGTGACCTTGGCCCC 420  
Db 361 GAAAAACAATCTCCAAAGCCAAAGGGGAGCCCGGAGAAACAAGGTGACCTTGGCCCC 420  
QY 421 ATCCGGGATGAGCTGACCAAGAACAGAGTCAAGCTGACCTGCTGCTCAAGGCTTTCTA 480  
Db 421 ATCCGGGATGAGCTGACCAAGAACAGAGTCAAGCTGACCTGCTGCTCAAGGCTTTCTA 480  
QY 481 TCCGACGACATCCCGCTGAGTGGAGAGCAATGGGCAAGCCGAGAAACAATCAAGAC 540  
Db 481 TCCGACGACATCCCGCTGAGTGGAGAGCAATGGGCAAGCCGAGAAACAATCAAGAC 540  
QY 541 CAGGCTCCCGTGTGAGTCTCCGACGGCTCTTCTTCTCTCAAGCAAGCTCAAGGTGA 600  
Db 541 CAGGCTCCCGTGTGAGTCTCCGACGGCTCTTCTTCTCTCAAGCAAGCTCAAGGTGA 600  
QY 601 CAAGAGAGGTGGCAGCAGGAGGAGAAAGTCTTCTCAAGCTGATGATGAGGCTCTGCA 660  
Db 601 CAAGAGAGGTGGCAGCAGGAGGAGAAAGTCTTCTCAAGCTGATGATGAGGCTCTGCA 660  
QY 661 CAACCACTACACGCAAGAAAGCTCTCTCTGCTCCGGGCTGCAACTGAGCAAGACCTG 720  
Db 661 CAACCACTACACGCAAGAAAGCTCTCTCTGCTCCGGGCTGCAACTGAGCAAGACCTG 720  
QY 721 TGCTGAGGCCCAAGAGCGGGAGCTGAGCGGCTCTGAGCAAGCATCC 768  
Db 721 TGCTGAGGCCCAAGAGCGGGAGCTGAGCGGCTCTGAGCAAGCATCC 768

RESULT 2  
ARI66804  
LOCUS ARI66804 768 bp DNA linear PAT 17-OCT-2001  
DEFINITION Sequence 32 from patent US 6284240.  
ACCESSION ARI66804  
VERSION ARI66804.1 GI:16243146  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 768)  
TITLE Seed, B., Banapour, B., Romeo, C. and Kolanus, W.  
JOURNAL Targeted cytolytic of HIV-infected cells by chimeric CD4  
FEATURES  
SOURCE Patent: US 6284240-A 32 04-SEP-2001;  
Location/Qualifiers  
1..768  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 768; DB 6; Length 768;  
Best Local Similarity 100.0%; Pred. No. 1.1e-139;  
Matches 768; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGTAGCAGAGCCCAATCTTGTGACAAACCTACACAGTCCCGCCAGCACTGA 60  
Db 1 GGTAGCAGAGCCCAATCTTGTGACAAACCTACACAGTCCCGCCAGCACTGA 60  
QY 61 ACTCCGGGGGAGCCGTCACTCTCTCTTCCCGCCAAACCAAGACACCTCATGAT 120  
Db 61 ACTCCGGGGGAGCCGTCACTCTCTCTTCCCGCCAAACCAAGACACCTCATGAT 120  
QY 121 CTCCCGGAGCCCTGAGTCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 180  
Db 121 CTCCCGGAGCCCTGAGTCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 180

QY 181 CAAGTTCACTGTAAGTGGACGCGCTGAGAGTGCATTAATGCCAAGCAAGCCGGGGA 240  
Db 181 CAAGTTCACTGTAAGTGGACGCGCTGAGAGTGCATTAATGCCAAGCAAGCCGGGGA 240  
QY 241 GGAGCAGTACCAAGCAGTACCGGGGTGACAGTCTTCAACCTGTCACACAGACTG 300  
Db 241 GGAGCAGTACCAAGCAGTACCGGGGTGACAGTCTTCAACCTGTCACACAGACTG 300  
QY 301 GCTGAATGGCAAGAGTACAAAGTGCACAAAGCCCTCCAGGCCCATGCA 360  
Db 301 GCTGAATGGCAAGAGTACAAAGTGCACAAAGCCCTCCAGGCCCATGCA 360  
QY 361 GAAAAACATCTCCAAAGCCAAAGGGGAGCCCGGAGAAACAAGGTGACCTTGGCCCC 420  
Db 361 GAAAAACATCTCCAAAGCCAAAGGGGAGCCCGGAGAAACAAGGTGACCTTGGCCCC 420  
QY 421 ATCCGGGATGAGCTGACCAAGAACAGAGTCAAGCTGACCTGCTGCTCAAGGCTTTCTA 480  
Db 421 ATCCGGGATGAGCTGACCAAGAACAGAGTCAAGCTGACCTGCTGCTCAAGGCTTTCTA 480  
QY 481 TCCGACGACATCCCGCTGAGTGGAGAGCAATGGGCAAGCCGAGAAACAATCAAGAC 540  
Db 481 TCCGACGACATCCCGCTGAGTGGAGAGCAATGGGCAAGCCGAGAAACAATCAAGAC 540  
QY 541 CAGGCTCCCGTGTGAGTCTCCGACGGCTCTTCTTCTCTCAAGCAAGCTCAAGGTGA 600  
Db 541 CAGGCTCCCGTGTGAGTCTCCGACGGCTCTTCTTCTCTCAAGCAAGCTCAAGGTGA 600  
QY 601 CAAGAGAGGTGGCAGCAGGAGGAGAAAGTCTTCTCAAGCTGATGATGAGGCTCTGCA 660  
Db 601 CAAGAGAGGTGGCAGCAGGAGGAGAAAGTCTTCTCAAGCTGATGATGAGGCTCTGCA 660  
QY 661 CAACCACTACACGCAAGAAAGCTCTCTCTGCTCCGGGCTGCAACTGAGCAAGACCTG 720  
Db 661 CAACCACTACACGCAAGAAAGCTCTCTCTGCTCCGGGCTGCAACTGAGCAAGACCTG 720  
QY 721 TGCTGAGGCCCAAGAGCGGGAGCTGAGCGGCTCTGAGCAAGCATCC 768  
Db 721 TGCTGAGGCCCAAGAGCGGGAGCTGAGCGGCTCTGAGCAAGCATCC 768

RESULT 3  
ARS60090  
LOCUS ARS60090 768 bp mRNA linear PAT 08-OCT-2004  
DEFINITION Sequence 32 from patent US 6753162.  
ACCESSION ARS60090  
VERSION ARS60090.1 GI:53970430  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 768)  
TITLE Seed, B., Banapour, B., Romeo, C. and Kolanus, W.  
JOURNAL Targeted cytolytic of HIV-infected cells by chimeric CD4  
FEATURES  
SOURCE Patent: US 6753162-A 32 22-JUN-2004;  
Location/Qualifiers  
1..768  
/organism="unknown"  
/mol\_type="mRNA"

ORIGIN  
Query Match 100.0%; Score 768; DB 6; Length 768;  
Best Local Similarity 100.0%; Pred. No. 1.1e-139;  
Matches 768; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGTAGCAGAGCCCAATCTTGTGACAAACCTACACAGTCCCGCCAGCACTGA 60  
Db 1 GGTAGCAGAGCCCAATCTTGTGACAAACCTACACAGTCCCGCCAGCACTGA 60  
QY 61 ACTCTGGGGGAGCCGTCACTCTCTTCCCGCCAAACCAAGAGACCTCATGAT 120  
Db 61 ACTCTGGGGGAGCCGTCACTCTCTTCCCGCCAAACCAAGAGACCTCATGAT 120

```

QY 121 CTCCTGGGACCCCTGAGGTCAATGCGGCTGCTGAGAGCGACGAGACCCCTGAGGT 180
DB 121 CTCCTGGGACCCCTGAGGTCAATGCGGCTGCTGAGAGCGACGAGACCCCTGAGGT 180
QY 181 CAAGTTCAATGCTAGCTGAGACGGCGCTGAGAGTGCATATATGCCAAGACCGCGGGA 240
DB 181 CAAGTTCAATGCTAGCTGAGACGGCGCTGAGAGTGCATATATGCCAAGACCGCGGGA 240
QY 241 GAGGAGTACACACGACGCTACCGGCTGCTGAGCTCTTCAACCGTCTCTGACACGAGCTG 300
DB 241 GAGGAGTACACACGACGCTACCGGCTGCTGAGCTCTTCAACCGTCTCTGACACGAGCTG 300
QY 301 GGTGAATGGCAAGAGTACAAAGTGCATGCTCCAAACAAAGCCCTCCAGCCCGCATGGA 360
DB 301 GGTGAATGGCAAGAGTACAAAGTGCATGCTCCAAACAAAGCCCTCCAGCCCGCATGGA 360
QY 361 GAAACCATCTCCAAAGCCAAAGGCGACGCCCGAGAACCAAGGTGTACACCTGCCCCC 420
DB 361 GAAACCATCTCCAAAGCCAAAGGCGACGCCCGAGAACCAAGGTGTACACCTGCCCCC 420
QY 421 ATCCCGGATGAGTGCACCAAGAACCGGTGACGCTTGAACCTGCTGCTCAAGGCTTCTA 480
DB 421 ATCCCGGATGAGTGCACCAAGAACCGGTGACGCTTGAACCTGCTGCTCAAGGCTTCTA 480
QY 481 TCCGAGGACATGCGCGTGGAGTGGAGAGCAATGGGACGCGGAGAACCACTACAAAGAC 540
DB 481 TCCGAGGACATGCGCGTGGAGTGGAGAGCAATGGGACGCGGAGAACCACTACAAAGAC 540
QY 541 CAGCGCTCCCGTCTGAGCTCCGACGCGCTCTTCTCTTCTACAGCAAGCTCACCGTGA 600
DB 541 CAGCGCTCCCGTCTGAGCTCCGACGCGCTCTTCTCTTCTACAGCAAGCTCACCGTGA 600
QY 601 CAAGAGAGGTGGAGAGAGGAGAAAGCTTCTCTCATGCTCCGTGATGATGAGGCTCTGCA 660
DB 601 CAAGAGAGGTGGAGAGAGGAGAAAGCTTCTCTCATGCTCCGTGATGATGAGGCTCTGCA 660
QY 661 CAACCACTACAGCAGAGAGAGCGCTCTGCTGCTGCGGGGCTGCACTGAGACGAGACTG 720
DB 661 CAACCACTACAGCAGAGAGAGCGCTCTGCTGCTGCGGGGCTGCACTGAGACGAGACTG 720
QY 721 TGCTGAGGCCCAAGACGCGGAGCTGAGCGGAGCTCTGAGACGAGACTG 768
DB 721 TGCTGAGGCCCAAGACGCGGAGCTGAGCGGAGCTCTGAGACGAGACTG 768

```

**RESULT 4**  
**LOCUS** BC019046 3134 bp mRNA linear PRI 06-OCT-2003  
**DEFINITION** Homo sapiens cDNA clone MGC:20691 IMAGE:4766140, complete cds.  
**ACCESSION** BC019046  
**VERSION** BC019046.2 GI:33879071  
**KEYWORDS** MGC.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
**REFERENCE** 1 (bases 1 to 3134)  
**AUTHORS** Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klauener, R.D., Collins, F.S., Wagner, L., Shenner, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loguigliano, N.A., Peters, G.J., Abramson, R.D., Muliyil, S.J., Bosnak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.D., Hult, S.W., Villalón, D.R., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Heltin, E., Kettner, M., Madan, A., Young, A.C., Shevchenko, Y., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

**TITLE** JOURNAL  
**MEDLINE** 22388257  
**PUBMED** 12477932  
**REFERENCE** 2 (bases 1 to 3134)  
**AUTHORS** Strausberg, R.  
**TITLE** Direct Submission  
**COMMENT** Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
**REMARK** NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
**COMMENT** On Aug 19, 2003 this sequence version replaced gi:17512135.  
**CONTACT** MGC help desk  
**EMAIL** [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
**TISSUE** Tissue Procurement: Louis Staudt  
**CDNA** CDNA Library Preparation: Rubin Laboratory  
**CDNA** CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
**DNA** DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),  
**SEQUENCING** Gaithersburg, Maryland;  
**WEB** Web site: <http://www.nisc.nih.gov/>  
**CONTACT** [nisc\\_mgc@hgrl.nih.gov](mailto:nisc_mgc@hgrl.nih.gov)  
**AKHTER** Akhter, N., Aylee, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Khong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masello, C., Maskeri, B., Massironi, S.D., McColoney, J.C., McDowell, J., Pearson, R., Stantipop, S., Thomas, P.J., Touchman, J.W., Tsugeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.  
**CLONE** Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
**SERIES** Series: IRL Plate: 30 Row: p Column: 3.  
**LOCATION** Location/Qualifiers  
**FEATURES** 1. 3134  
**SOURCE** /organism="Homo sapiens"  
**mol\_type**="mRNA"  
**db\_xref**="taxon:9606"  
**clone**="MGC:20691 IMAGE:4766140"  
**issue**="Primary B-Cells from Tonsils"  
**lab\_host**="DH10B-R"  
**note**="Vector: POTB7"  
**64**. 1698  
**codon\_start**=1  
**product**="Unknown (protein for MGC:20691)"  
**protein**="GI:17512136"  
**translation**="MEFGLSWVFLVALRNGVCOAQLVBSGGVVOGSSLRSLSCAS  
GPRFSNYGMWVQAPGKLEWAVFSYBSDSYVAVSAGRTISIDNSKRLSLQMS  
NSLRVDPLVYVCAKDKQKQVSNMSTGDRGRTIVYSSASRKGVPFLVAPS  
KTSRGCTALAGCLVADYFPPEPVYVSNRSGALTSQVTFPVLVDSGLVSLSVYPS  
SSLGDTYVLCNVNHRKSNTRKVDKVPKSCDKTHTCPCPAPLGGPSVFLPPPKK  
DTIMHRIETVEVTVVVDVSHEDPEVFNVDVENVNAKTKEREGQVNTYVAVSL  
TVLQHWMLNKEVCKYSNKALPALEKITSKACQGPABEQVTVTLPPSRDELTKQVVS  
LVCLVGVPSDIAVEMSGQEPNNYKTPPKVKGDSPEFLYSLKLVDSRWQGVN  
FSGVWHEALRHNYTKSISPELQLESCAQAQDGEIDGWTITITITFLPLSLVC  
YKATVTFPKKMTFSSVVDIKQTIIPIDYRMICQA"  
**169**. 411  
**note**="IGV: Region: Immunoglobulin V-Type"  
**db\_xref**="CDI:smatc00406"  
**562**. 759  
**note**="IGL: Region: Immunoglobulin C-Type"  
**db\_xref**="CDI:smatc00407"  
**922**. 1140  
**note**="IGL: Region: Immunoglobulin C-Type"  
**db\_xref**="CDI:smatc00407"

misc\_feature 1231..1452  
/note="IGC1; Region: Immunoglobulin C-Type"  
/db\_xref="CD: smart00407"

Query Match 97.0%; Score 744.6; DB 9; Length 3134;  
Best Local Similarity 98.8%; Pred. No. 3.4e-135;  
Matches 750; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 4 AGCAGAGCCCAATCTTGTGACAAACTCAGACATGCCACCGTGGCCAGACCTGAACT 63  
DB 789 AGTTGAGCCCAATCTTGTGACAAACTCAGACATGCCACCGTGGCCAGACCTGAACT 848  
QY 64 CTTGGGGGGACCGTCACTCTCTTCCGCCAAAACCAAGGACACCTCATATCTC 123  
DB 849 CTTGGGGGGACCGTCACTCTCTTCCGCCAAAACCAAGGACACCTCATATCTC 908  
QY 124 CCGGACCCCTGAGTGCATATGCTGTGTGTGAGCTGAGCCAGAAACCTTGAAGTCAA 183  
DB 909 CCGGACCCCTGAGTGCATATGCTGTGTGTGAGCTGAGCCAGAAACCTTGAAGTCAA 968  
QY 184 GTTCAACTGTGATCTGTGACGCGGTGAGGTGATTAATGCCAAAGCCGCGGAGGA 243  
DB 969 GTTCAACTGTGATCTGTGACGCGGTGAGGTGATTAATGCCAAAGCCGCGGAGGA 1028  
QY 244 GGAATGACCAACAGACGTAACCGGTGTGACGCTCTCAACGCTCTGACAGACTGACT 303  
DB 1029 GGAATGACCAACAGACGTAACCGGTGTGACGCTCTCAACGCTCTGACAGACTGACT 1088  
QY 304 GAATGGCAAGAGTACAGTGCAGAGGTCTCCAAAGAAACCTCCAGACCCCTCGAGAA 363  
DB 1089 GAATGGCAAGAGTACAGTGCAGAGGTCTCCAAAGAAACCTCCAGACCCCTCGAGAA 1148  
QY 364 AACCATCTCCAAAGCCAAAGGGGACGCCCGAGAAACAAGGTGACACCTGCCCCATC 423  
DB 1149 AACCATCTCCAAAGCCAAAGGGGACGCCCGAGAAACAAGGTGACACCTGCCCCATC 1208  
QY 424 CCGGAGATGAGTGCACAGAAACAGGTCAAGCTGACCTGTGTTCAAGGCTTTATTC 483  
DB 1209 CCGGAGATGAGTGCACAGAAACAGGTCAAGCTGACCTGTGTTCAAGGCTTTATTC 1268  
QY 484 CAGGACATGCGCTGTGAGTGGAGAGCAATGGGACGCGGAGAAACAATTAAGACCA 543  
DB 1269 CAGGACATGCGCTGTGAGTGGAGAGCAATGGGACGCGGAGAAACAATTAAGACCA 1328  
QY 544 GCGTCCCGTGTGACCTCGAAGGCTCTTCTCTTACAGAGCTCAACGTTGACAA 603  
DB 1329 GCGTCCCGTGTGACCTCGAAGGCTCTTCTCTTACAGAGCTCAACGTTGACAA 1388  
QY 604 GAGCAGGTGACAGAGGAAACGTCTTCTCATGCTCCGTGATGACATGAGGCTCTGACA 663  
DB 1389 GAGCAGGTGACAGAGGAAACGTCTTCTCATGCTCCGTGATGACATGAGGCTCTGACA 1448  
QY 664 CCACTACAGCGCAAGAAAGCTCTCTCTGCTCGGGGGCTGCAACTGAGACCTGTGC 723  
DB 1449 CCACTACAGCGCAAGAAAGCTCTCTCTGCTCGGGGGCTGCAACTGAGAGACTGTGC 1508  
QY 724 TGAAGCCCAAGAGCGGAGACTGACGAGGCTTGAACGAC 762  
DB 1509 GGAAGCCCAAGAGCGGAGACTGACGAGGCTTGAACGAC 1547

RESULT 5  
CO851090 3075 bp DNA Linear PAT 23-AUG-2004  
LOCUS CQ851090  
DEFINITION Sequence 1559 from Patent EP1447413.  
ACCESSION CQ851090  
VERSION CQ851090.1 GI:51509302  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Bukaryota; Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1  
AUTHORS Isegai, T., Yamamoto, J., Nishikawa, T., Isono, Y., Sugiyama, T.,  
Otsuki, T., Wakamatsu, A., Ishii, S., Nagai, K. and Irie, R.  
TITLE Full-length human CDNA  
JOURNAL Patent: EP 1447413-A 1559 18-AUG-2004;  
FEATURES  
source Research Association for Biotechnology (JP)  
1..3075  
location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 96.1%; Score 738.2; DB 6; Length 3075;  
Best Local Similarity 98.3%; Pred. No. 5.9e-134;  
Matches 746; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 4 AGCAGAGCCCAATCTTGTGACAAACTCAGACATGCCACCGTGGCCAGACCTGAACT 63  
DB 748 AGTTGAGCCCAATCTTGTGACAAACTCAGACATGCCACCGTGGCCAGACCTGAACT 807  
QY 64 CTTGGGGGGACCGTCACTCTCTTCCGCCAAAACCAAGGACACCTCATATCTC 123  
DB 808 CTTGGGGGGACCGTCACTCTCTTCCGCCAAAACCAAGGACACCTCATATCTC 867  
QY 124 CCGGACCCCTGAGTGCATATGCTGTGTGTGAGCTGAGCCAGAAACCTTGAAGTCAA 183  
DB 868 CCGGACCCCTGAGTGCATATGCTGTGTGTGAGCTGAGCCAGAAACCTTGAAGTCAA 927  
QY 184 GTTCAACTGTGATCTGTGACGCGGTGAGGTGATTAATGCCAAAGCCGCGGAGGA 243  
DB 928 GTTCAACTGTGATCTGTGACGCGGTGAGGTGATTAATGCCAAAGCCGCGGAGGA 987  
QY 244 GCAATGACCAACAGACGTAACCGGTGTGACGCTCTCAACGCTCTGACAGACTGACT 303  
DB 988 GCAATGACCAACAGACGTAACCGGTGTGACGCTCTCAACGCTCTGACAGACTGACT 1047  
QY 304 GAATGGCAAGAGTACAGTGCAGAGGTCTCCAAAGAAACCTCCAGACCCCTCGAGAA 363  
DB 1048 GAATGGCAAGAGTACAGTGCAGAGGTCTCCAAAGAAACCTCCAGACCCCTCGAGAA 1107  
QY 364 AACCATCTCCAAAGCCAAAGGGGACGCCCGAGAAACAAGGTGACACCTGCCCCATC 423  
DB 1108 AACCATCTCCAAAGCCAAAGGGGACGCCCGAGAAACAAGGTGACACCTGCCCCATC 1167  
QY 424 CCGGAGATGAGTGCACAGAAACAGGTCAAGCTGACCTGTGTTCAAGGCTTTATTC 483  
DB 1168 CCGGAGATGAGTGCACAGAAACAGGTCAAGCTGACCTGTGTTCAAGGCTTTATTC 1227  
QY 484 CAGGACATGCGCTGTGAGTGGAGAGCAATGGGACGCGGAGAAACAATTAAGACCA 543  
DB 1228 CAGGACATGCGCTGTGAGTGGAGAGCAATGGGACGCGGAGAAACAATTAAGACCA 1287  
QY 544 GCGTCCCGTGTGACCTCGAAGGCTCTTCTCTTACAGAGCTCAACGTTGACAA 603  
DB 1288 GCGTCCCGTGTGACCTCGAAGGCTCTTCTCTTACAGAGCTCAACGTTGACAA 1347  
QY 604 GAGCAGGTGACAGAGGAAACGTCTTCTCATGCTCCGTGATGACATGAGGCTCTGACA 663  
DB 1348 GAGCAGGTGACAGAGGAAACGTCTTCTCATGCTCCGTGATGACATGAGGCTCTGACA 1407  
QY 664 CCACTACAGCGCAAGAAAGCTCTCTCTGCTCGGGGGCTGCAACTGAGACCTGTGC 723  
DB 1408 CCACTACAGCGCAAGAAAGCTCTCTCTGCTCGGGGGCTGCAACTGAGAGACTGTGC 1467  
QY 724 TGAAGCCCAAGAGCGGAGACTGACGAGGCTTGAACGAC 762  
DB 1468 GGAAGCCCAAGAGCGGAGACTGACGAGGCTTGAACGAC 1506

RESULT 6  
AK128301 3075 bp mRNA Linear PRI 19-FEB-2004  
LOCUS AK128301

DEFINITION Homo sapiens cDNA FLJ46441 fis, clone THYMJ3016518, highly similar to Ig gamma-1 chain C region.  
ACCESSION AK128301  
VERSION AK128301.1 GI:34535606  
KEYWORDS oligo capping, file (full insert sequence).  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukutsumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Ohta, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai, H., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Waga, S., Murakawa, K., Kanemori, K., Takahashi, T., Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K., Masuno, Y., Nagai, K. and Isogai, T.  
TITLE NEDO human cDNA sequencing project  
JOURNAL Unpublished  
2 (base 1 to 3075)  
REFERENCE 2  
AUTHORS Isogai, T. and Yamamoto, J.  
TITLE Direct Submision  
JOURNAL Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamata, Kisarazu, Chiba 292-0818, Japan  
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB) (supported by Japan Construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5' & 3'-end one pass sequencing: RAB, HRI and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: Reverse Proteomics Research Institute, HRI and RAB.

FEATURES  
source  
1. .3075  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="THYMJ3016518"  
/issue\_type="thymus"  
/clone\_id="THYMJ3"  
/note="cloning vector: pME18SFL3"  
38.1657  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="BAC87374.1"  
/db\_xref="GI:34535607"  
/translation="MERGLSWLFLVALILKQVCEVQLDSGGGLVORGGSLRLCAAS  
EFTFRDAMHWRQAFPEGLQWVSGISQOSTWYDVSGRFTISKDSENTYIQM  
NSLRADTAVYCAKDMGVTRSRYPDWGGGLVAASASTKGSVPEPLAPSSKTSIG  
GTALGLVDVPEPEPTVSWNSGALTSVGHPTPAVLQSGLSLVSVVPSLSIGT  
QYICVNHKPSNTKYDKRVKSPKCDKTHCPSPAPELLGSGSVFLFPKPDQTLMI  
SRPEVTCVVDVSHDPEVRFNMVYGVVNAKTPREQVNSTRVVSVLTVLH  
DMNGEYKCKVKNKALPARIETKISAKQPREPOVYTLPRERETKQVSLTCLV  
KGYPSDIAVEMESNGQPENNYKTPPVLDSDSPFLYSGLTYDKSKMOQGNFSCV  
MHRALNHYQKSLSPQLQBSCEADGSLDGLMTITTTITLFLSLVCSATV  
TPEKVKWIFSSVVDLKTITIPYRMIGQA"

CDS  
38.1657  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="BAC87374.1"  
/db\_xref="GI:34535607"  
/translation="MERGLSWLFLVALILKQVCEVQLDSGGGLVORGGSLRLCAAS  
EFTFRDAMHWRQAFPEGLQWVSGISQOSTWYDVSGRFTISKDSENTYIQM  
NSLRADTAVYCAKDMGVTRSRYPDWGGGLVAASASTKGSVPEPLAPSSKTSIG  
GTALGLVDVPEPEPTVSWNSGALTSVGHPTPAVLQSGLSLVSVVPSLSIGT  
QYICVNHKPSNTKYDKRVKSPKCDKTHCPSPAPELLGSGSVFLFPKPDQTLMI  
SRPEVTCVVDVSHDPEVRFNMVYGVVNAKTPREQVNSTRVVSVLTVLH  
DMNGEYKCKVKNKALPARIETKISAKQPREPOVYTLPRERETKQVSLTCLV  
KGYPSDIAVEMESNGQPENNYKTPPVLDSDSPFLYSGLTYDKSKMOQGNFSCV  
MHRALNHYQKSLSPQLQBSCEADGSLDGLMTITTTITLFLSLVCSATV  
TPEKVKWIFSSVVDLKTITIPYRMIGQA"

ORIGIN  
Query Match 96.1%; Score 738.2; DB 9; Length 3075;  
Best Local Similarity 98.3%; Pred. No. 5.9e-134;  
Matches 746; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 4 AGCAGAGCCCAATCTGTGACAACTGACACATGCCACCGTCCAGACACTGACT 63  
Db 748 AGTTGAGCCCAATCTGTGACAACTGACACATGCCACCGTCCAGACACTGACT 807

QY 64 CTTGGGGGAGACCGTCACTCTTCTTCCCGGCAAAACCAAGACACCTCATGATTC 123  
Db 808 CTTGGGGGAGACCGTCACTCTTCTTCCCGGCAAAACCAAGACACCTCATGATTC 867

QY 124 CCGGACCCCTGAGTCAATGCTGTGTGTGACGTGAGCCAGAAACCTTGAGTCA 183  
Db 868 CCGGACCCCTGAGTCAATGCTGTGTGTGACGTGAGCCAGAAACCTTGAGTCA 927

QY 184 GTTCAACTGAGTCACTGACCGGCTGAGAGGTGCTAATGCCAGACAAAGCCGGAGGA 243  
Db 928 GTTCAACTGAGTCACTGACCGGCTGAGAGGTGCTAATGCCAGACAAAGCCGGAGGA 987

QY 244 GCAGTCAACAGACGTCACCGGCTGTGACCGGCTGTGACCGGCTGTGACCGGCTGTGAC 303  
Db 988 GCAGTCAACAGACGTCACCGGCTGTGACCGGCTGTGACCGGCTGTGACCGGCTGTGAC 1047

QY 304 GAATGCAAGAGTCAAGTCAAGTCTTCAACAAAGCCCTCCAGCCCTCCAGAGAA 363  
Db 1048 GAATGCAAGAGTCAAGTCAAGTCTTCAACAAAGCCCTCCAGCCCTCCAGAGAA 1107

QY 364 AACCATCTCCAAAGCCAAAGGAGGAGCCCGAGAACCAAGTGTACACCTGCCCCATC 423  
Db 1108 AACCATCTCCAAAGCCAAAGGAGGAGCCCGAGAACCAAGTGTACACCTGCCCCATC 1167

QY 424 CCGGATGAGTCAACCAAGACCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 483  
Db 1168 CCGGATGAGTCAACCAAGACCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1227

QY 484 CAGGACATGCGCGTGAAGTGAAGCAATGAGGACCGGAGAACCAATCAAGACAC 543  
Db 1228 CAGGACATGCGCGTGAAGTGAAGCAATGAGGACCGGAGAACCAATCAAGACAC 1287

QY 544 GCTCTCCGTGTGAGTCCGACGCGCTCTTCTTCTTCAAGCAAGTCAAGTCAAGTCAAGTCA 603  
Db 1288 GCTCTCCGTGTGAGTCCGACGCGCTCTTCTTCTTCAAGCAAGTCAAGTCAAGTCAAGTCA 1347

QY 604 GAGCAGTGCAGCAGGAGAAAGTCTTCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 663  
Db 1348 GAGCAGTGCAGCAGGAGAAAGTCTTCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1407

QY 664 CCACTACAGCAGAAAGCTCTCTCTGCTCCGAGCTGCAACTGACGACCTGTGC 723  
Db 1408 CCACTACAGCAGAAAGCTCTCTCTGCTCCGAGCTGCAACTGACGACCTGTGC 1467

QY 724 TGAAGCCCAAGACCGGAGAGTGAAGCGGCTGTGAGCAGC 762  
Db 1468 TGAAGCCCAAGACCGGAGAGTGAAGCGGCTGTGAGCAGC 1506

RESULT 7  
Q0851340  
LOCUS Q0851340 3183 bp DNA linear PAT 23-AUG-2004  
DEFINITION Sequence 1809 from Patent EP1447413.  
ACCESSION Q0851340  
VERSION Q0851340.1 GI:51509552  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Isogai, T., Yamamoto, J., Nishikawa, T., Isono, Y., Sugiyama, T., Otsuki, T., Wakamatsu, A., Ishii, S., Nagai, K. and Irie, R.  
TITLE Full-length human cDNA  
JOURNAL Patent: EP 1447413-A 1809 18-AUG-2004;  
Research Association for Biotechnology (JP)  
FEATURES  
source  
1. .3183  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 91.3%; Score 701; DB 6; Length 3183;  
Best Local Similarity 95.4%; Pred. No. 1.1e-126;  
Matches 722; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

```

QY 6 CAGAGCCCAATCTTGTGACAAAATGACATGCGCCACCGTGGCCAGACCTGAATCC 65
Db 866 CAGAGCCCAATCTTGTGACAAAATGACATGCGCCACCGTGGCCAGACCTGAATCC 925
QY 66 TGGGGGAGACCGTCAAGTCTTCTCTTCCCGCCAAAACCAAGACACCCCTGATGATCTCC 125
Db 926 TGGGAGAGACCGTCAAGTCTTCTCTTCCCGCCAAAACCAAGATACCTTATGATTTTCC 985
QY 126 GGAACCCCTGAGGTGACATGCGTGGTGTGAGCGTGAAGCCAGAAAGACCTGAGGTCAAGT 185
Db 986 GGAACCCCTGAGGTGACATGCGTGGTGTGAGCGTGAAGCCAGAAAGACCTGAGGTCAAGT 1045
QY 186 TCAACTGTGACGTGACGCGGTGAGGTGACATAATGCAAGACAAAGCCGGGAGAGC 245
Db 1046 TCAAGTGTGACGTGACGCGGTGAGGTGACATAATGCAAGACAAAGCCGGGAGAGC 1105
QY 246 AGTACAAAGACGACGTCAGCGGTGTGTCAGCGTCTTCAACCGTCTGACACAGACCTGCTGA 305
Db 1106 AGTACAAAGACGACGTCAGCGGTGTGTCAGCGTCTTCAACCGTCTGACACAGACCTGCTGA 1165
QY 306 ATGGCAAGAGGTACAAATGCAAGGTCTTCCAAACAAAGCCCTCCAGCCCATGAGAAA 365
Db 1166 ACAGCAAGAGGTACAAATGCAAGGTCTTCCAAACAAAGCCCTCCAGCCCATGAGAAA 1225
QY 366 CCAATCTTCAAAAGCCAAAGGCGACGCCCGAAGACCAAGGTGACACCCCTGCCCCATCCC 425
Db 1226 CCAATCTTCAAAAGCCAAAGGCGACGCCCGAAGACCAAGGTGACACCCCTGCCCCATCCC 1285
QY 426 GGGATGAGTGTACCAAGACCAAGTCAAGCTGACCTGCTGTCAAAAGGCTTATCCCA 485
Db 1286 GGGATGAGTGTACCAAGACCAAGTCAAGCTGACCTGCTGTCAAAAGGCTTATCCCA 1345
QY 486 GGGACATGCGCGGTGAGGTGAGAGCAATGGGACGCGGAGAACATTAAGACCAAGC 545
Db 1346 GGGACATGCGCGGTGAGGTGAGAGCAATGGGACGCGGAGAACATTAAGACCAAGC 1405
QY 546 CTCCTGCTGAGTCTCGACGCGTCTTCTTCTCTTCAAGACGCTCAACCGTGAAGAA 605
Db 1406 CTCCTGCTGAGTCTCGACGCGTCTTCTTCTCTTCAAGACGCTCAACCGTGAAGAA 1465
QY 606 GCGAGGTGAGCAGCGGGAGCGTCTTCTCATGCTCCGATGACATGAGGCTTGCACAAAC 665
Db 1466 GCGAGGTGAGCAGCGGGAGCGTCTTCTCATGCTCCGATGACATGAGGCTTGCACAAAC 1525
QY 666 ACTACACGAGAGAGCGTCTCTCTGCTCCGCGGGCTGCAACGAGACCTGTGCTG 725
Db 1526 GCTTACGAGAGAGCGTCTCTCTGCTCCGAGGCTGCAACGAGACCTGTGCTG 1585
QY 726 AGGCGCAGAGCGGGAGCGTGAAGCGGCTCTGACGAC 762
Db 1586 AGGCGCAGAGCGGGAGCGTGAAGCGGCTCTGACGAC 1622

```

```

RESULT 8
AKI28579 3183 bp mRNA linear PRI 19-FEB-2004
LOCUS Homo sapiens cDNA FLJ46738 fis, clone TRACH3020930, highly similar
DEFINITION to IG gamma-1 chain C region.
ACCESSION AKI28579
VERSION AKI28579.1 GI:34536019
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

```

```

REFERENCE
AUTHORS Kanehori,K., Ishibashi,T., Chiba,Y., Fujimori,K., Hiraoka,S., Tanai,H.,
Watanabe,S., Ishida,S., Ono,Y., Horiuta,T., Watanabe,M., Sugiyama,T.,
Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A., Ishii,S., Yamamoto,J.,
Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Matsuo,K.,
Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A.,
Oshina,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K.,

```

```

TITLE Masuo,Y., Nagai,K. and Isogai,T.
JOURNAL NEDO human cDNA sequencing project
REFERENCE 2 (bases 1 to 3183)
AUTHORS Isogai,T. and Yamamoto,J.
TITLE Direct Submission
JOURNAL Submitted (15-JUN-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'-3' end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: Reverse Proteomics Research Institute, HRI and RAB.

FEATURES
source
    location/Qualifiers
        1..3183
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="TRACH3020930"
            /tissue_type="trachea"
            /clone_id="TRACH3"
            /note="cloning vector: pME18SFL3"
            40..1173
                /note="unnamed protein product"
                /codon_start=1
                /protein_id="BAC87509.1"
                /db_xref="GI:34536020"
                /translation="MKHLMPFLYLAARWVLSQVLOSGRLVKPSFVSLTGVSDSISRGYVSWIRQPAKGLSEWIGRAVITGTFTYNSFKRVTISASFKELISLEINSLTAADATATYFCAREMGPQWGSNDAPETWQGLIVSPASTGSPVLSVATVPSSTSGGTALALCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGHYSLSSVTVPSLSLTQVYTCNVNKKPSMTKVDKVELEPLGDTHTCPKPREPKSDTPEPCRCPEKSDDTPEPCRCPPALPELGSVFLPPEPKKDTLMSRPETVCVVVDVSHEDPEVDPKWDVGGVCHVNAATKPREPQNSPTFVSVSTLTJLHODMNGSKYKKYKSKALPAPTEKTSKTKGQPREPOVYTLPPSRREEMTKNQVSLTCLVKGFPSPIAIVWESGQPENNTNTPPMIDSDGSFPLYSKLTIVDSRWQGNIFGCSVWHEALNHRFTQKSLSPETQLSESCAEKADDELGLMTTITITIFITLFLSVCSATVYFFKWKVIFSSVDLKOTIIPYRMWIGGA"

ORIGIN
Query Match 91.3%; Score 701; DB 9; Length 3183;
Best Local Similarity 95.4%; Pred. No. 1.1e-126;
Matches 722; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 6 CAGAGCCCAATCTTGTGACAAAATGACATGCGCCACCGTGGCCAGACCTGAATCC 65
Db 866 CAGAGCCCAATCTTGTGACAAAATGACATGCGCCACCGTGGCCAGACCTGAATCC 925
QY 66 TGGGGGAGACCGTCAAGTCTTCTCTTCCCGCCAAAACCAAGACACCCCTGATGATCTCC 125
Db 926 TGGGAGAGACCGTCAAGTCTTCTCTTCCCGCCAAAACCAAGATACCTTATGATTTTCC 985
QY 126 GGAACCCCTGAGGTGACATGCGTGGTGTGAGCGTGAAGCCAGAAAGACCTGAGGTCAAGT 185
Db 986 GGAACCCCTGAGGTGACATGCGTGGTGTGAGCGTGAAGCCAGAAAGACCTGAGGTCAAGT 1045
QY 186 TCAACTGTGACGTGACGCGGTGAGGTGACATAATGCAAGACAAAGCCGGGAGAGC 245
Db 1046 TCAAGTGTGACGTGACGCGGTGAGGTGACATAATGCAAGACAAAGCCGGGAGAGC 1105
QY 246 AGTACAAAGACGACGTCAGCGGTGTGTCAGCGTCTTCAACCGTCTGACACAGACCTGCTGA 305
Db 1106 AGTACAAAGACGACGTCAGCGGTGTGTCAGCGTCTTCAACCGTCTGACACAGACCTGCTGA 1165
QY 306 ATGGCAAGAGGTACAAATGCAAGGTCTTCCAAACAAAGCCCTCCAGCCCATGAGAAA 365
Db 1166 ACAGCAAGAGGTACAAATGCAAGGTCTTCCAAACAAAGCCCTCCAGCCCATGAGAAA 1225

```





RESULT 10  
CQ768745 7427 bp DNA linear PAT 04-MAR-2004  
LOCUS CQ768745  
DEFINITION Sequence 13 from Patent WO2004006962.  
ACCESSION CQ768745  
VERSION CQ768745.1 GI:45111935  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 b) Rn,S.R., Nicolaisen,E.M. and Steenstrup,T.D.  
A tissue factor binding immunocoujugate comprising factor vlla  
Patent: WO 2004006962-A 13 22-JAN-2004;  
NOVO NORDISK A/S (DK)  
FEATURES  
source  
Location/Qualifiers  
1..7427  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Description of Artificial Sequence:Artificial"

Query Match 90.5%; Score 695.2; DB 6; Length 7427;  
Best Local Similarity 98.2%; Pred. No. 1.3e-125;  
Matches 703; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

5 GCAGAGCCCAATCTTGTGCAAACTCAGACATGCGCCAGCCGCACTGAATC 64  
1349 GCAGAGCCCAATCTTGTGCAAACTCAGACATGCGCCAGCCGCACTGAATC 1408  
65 CTGGGGGAGACCGTCACTCTTCTTCCCGCAAAACCAAGACACCTCATATCTCC 124  
1409 CTGGGGGAGACCGTCACTCTTCTTCCCGCAAAACCAAGACACCTCATATCTCC 1468  
125 CGAACCCCTGAGGTGACATGCTGTGTGACGTGAGCCAGAGACCTTGAAGTCAAG 184  
1469 CGAACCCCTGAGGTGACATGCTGTGTGACGTGAGCCAGAGACCTTGAAGTCAAG 1528  
185 TTCAACTGTGACGTGAGCGGTGAGGTGATATGCAAGCAAAAGCCGGAGAGAG 244  
1529 TTCAACTGTGACGTGAGCGGTGAGGTGATATGCAAGCAAAAGCCGGAGAGAG 1588  
245 CAGTCAACAGACGATACCGGTGTCTCAACGCTCTCTGACAGCACTGGCTG 304  
1589 CAGTCAACAGACGATACCGGTGTCTCAACGCTCTCTGACAGCACTGGCTG 1648  
305 AATGGCAAGAGTACAGGTGACGTCTCAACAAAGCCCTCCAGCCCTCATGAGAA 364  
1649 AATGGCAAGAGTACAGGTGACGTCTCAACAAAGCCCTCCAGCCCTCATGAGAA 1708  
365 ACCATCTCCAAAGCCAAAGGCGACCCCGAGAACCAAGGTGACACCTGCCCCATCC 424  
1709 ACCATCTCCAAAGCCAAAGGCGACCCCGAGAACCAAGGTGACACCTGCCCCATCC 1768  
425 CGGATGAGTGAACAAGACAGGTCACTGACCTGCTGCTGCTCAAAAGCTTCTATCC 484  
1769 CGGATGAGTGAACAAGACAGGTCACTGACCTGCTGCTGCTCAAAAGCTTCTATCC 1828  
485 AGCGACATGCGCGTGAAGTGAAGCAATGGGACCGGAGAACCAATGACAGCAAG 544  
1829 AGCGACATGCGCGTGAAGTGAAGCAATGGGACCGGAGAACCAATGACAGCAAG 1888  
545 CCTCCCGTGTGAGCTCCGACCGCTCTTCTTCTCAACAGAGTCAACCTGAGCAAG 604  
1889 CCTCCCGTGTGAGCTCCGACCGCTCTTCTTCTCAACAGAGTCAACCTGAGCAAG 1948  
605 AGCAGGTGACAGAGGAGAACTTCTGATGCTCGGTGATGATGAGGCTCTGCAAC 664  
1949 AGCAGGTGACAGAGGAGAACTTCTGATGCTCGGTGATGATGAGGCTCTGCAAC 2008  
665 CACTTCAAGCAGAGAGGCTCTCTCTGCTCGGGGCTGCACTGACAGCACTG 720  
|||||

Db 2009 CACTTCAAGCAGAGAGGCTCTCTCTGCTCGGGGCTGCACTGACAGCACTG 2064  
RESULT 11  
CQ768742 7493 bp DNA linear PAT 04-MAR-2004  
LOCUS CQ768742  
DEFINITION Sequence 10 from Patent WO2004006962.  
ACCESSION CQ768742  
VERSION CQ768742.1 GI:45111927  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 b) Rn,S.R., Nicolaisen,E.M. and Steenstrup,T.D.  
A tissue factor binding immunocoujugate comprising factor vlla  
Patent: WO 2004006962-A 10 22-JAN-2004;  
NOVO NORDISK A/S (DK)  
FEATURES  
source  
Location/Qualifiers  
1..7493  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Description of Artificial Sequence:Artificial"

Query Match 90.5%; Score 695.2; DB 6; Length 7493;  
Best Local Similarity 98.2%; Pred. No. 1.3e-125;  
Matches 703; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

5 GCAGAGCCCAATCTTGTGCAAACTCAGACATGCGCCAGCCGCACTGAATC 64  
1415 GCAGAGCCCAATCTTGTGCAAACTCAGACATGCGCCAGCCGCACTGAATC 1474  
65 CTGGGGGAGACCGTCACTCTTCTTCCCGCAAAACCAAGACACCTCATATCTCC 124  
1475 CTGGGGGAGACCGTCACTCTTCTTCCCGCAAAACCAAGACACCTCATATCTCC 1534  
125 CGAACCCCTGAGGTGACATGCTGTGTGACGTGAGCCAGAGACCTTGAAGTCAAG 184  
1535 CGAACCCCTGAGGTGACATGCTGTGTGACGTGAGCCAGAGACCTTGAAGTCAAG 1594  
185 TTCAACTGTGACGTGAGCGGTGAGGTGATATGCAAGCAAAAGCCGGAGAGAG 244  
1595 TTCAACTGTGACGTGAGCGGTGAGGTGATATGCAAGCAAAAGCCGGAGAGAG 1654  
245 CAGTCAACAGACGATACCGGTGTCTCAACGCTCTCTGACAGCACTGGCTG 304  
1655 CAGTCAACAGACGATACCGGTGTCTCAACGCTCTCTGACAGCACTGGCTG 1714  
305 AATGGCAAGAGTACAGGTGACGTCTCAACAAAGCCCTCCAGCCCTCATGAGAA 364  
1715 AATGGCAAGAGTACAGGTGACGTCTCAACAAAGCCCTCCAGCCCTCATGAGAA 1774  
365 ACCATCTCCAAAGCCAAAGGCGACCCCGAGAACCAAGGTGACACCTGCCCCATCC 424  
1775 ACCATCTCCAAAGCCAAAGGCGACCCCGAGAACCAAGGTGACACCTGCCCCATCC 1834  
425 CGGATGAGTGAACAAGACAGGTCACTGACCTGCTGCTGCTCAAAAGCTTCTATCC 484  
1835 CGGATGAGTGAACAAGACAGGTCACTGACCTGCTGCTGCTCAAAAGCTTCTATCC 1894  
485 AGCGACATGCGCGTGAAGTGAAGCAATGGGACCGGAGAACCAATGACAGCAAG 544  
1895 AGCGACATGCGCGTGAAGTGAAGCAATGGGACCGGAGAACCAATGACAGCAAG 1954  
545 CCTCCCGTGTGAGCTCCGACCGCTCTTCTTCTCAACAGAGTCAACCTGAGCAAG 604  
1955 CCTCCCGTGTGAGCTCCGACCGCTCTTCTTCTCAACAGAGTCAACCTGAGCAAG 2014  
605 AGCAGGTGACAGAGGAGAACTTCTGATGCTCGGTGATGATGAGGCTCTGCAAC 664  
2015 AGCAGGTGACAGAGGAGAACTTCTGATGCTCGGTGATGATGAGGCTCTGCAAC 2074  
|||||



QY 665 CACTACACGAGAGAGCCCTCTCCCTGTCTCCGGGGCTGCATGAGACGACCTG 720  
Db 2075 CACTACACGAGAGAGCCCTCTCCCTGTCTCCGGGTAAATGAAGAGCGAATTCTG 2130

RESULT 12  
AX556949 1413 bp DNA linear PAT 27-NOV-2002  
LOCUS Sequence 4 from Patent WO02060955.  
DEFINITION AX556949  
ACCESSION AX556949.1 GI:25900012  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE  
1 Braeslawsky, G.R., Hanna, N. and Chinn, P.  
AUTHORS Modified antibodies and methods of use  
TITLE Patent: WO 02060955-A 4 08-AUG-2002;  
JOURNAL Idex Pharmaceuticals Corporation (US)  
FEATURES  
source 1..1413  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Humanized C2B8 Heavy Chain Sequence"

ORIGIN

Query Match 90.4%; Score 694.4; DB 6; Length 1413;  
Best Local Similarity 99.9%; Pred. No. 2.3e-125;  
Matches 695; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 AGCAGAGCCCAATCTTGTGACAAACTCAACATGCCCGTCCAGACCTGAACT 63  
Db 711 AGCAGAGCCCAATCTTGTGACAAACTCAACATGCCCGTCCAGACCTGAACT 770

QY 64 CCGGGGGGAGCGTCAGTCTTCTTCCCGCCCAAAACCAAGAGACCTCATGATCTC 123  
Db 771 CCGGGGGGAGCGTCAGTCTTCTTCCCGCCCAAAACCAAGAGACCTCATGATCTC 830

QY 124 CCGGACCCCTGAGGTCAATGCTGTGTGACGTGAGCCAGAAACCTTGAGGTCA 183  
Db 831 CCGGACCCCTGAGGTCAATGCTGTGTGAGGTGAGCCAGAAACCTTGAGGTCA 890

QY 184 GTTCAACTGTGACGTGAGCGGCTGTGAGGTGATATGCAAGCAAAAGCCGGAGGA 243  
Db 891 GTTCAACTGTGACGTGAGCGGCTGTGAGGTGATATGCAAGCAAAAGCCGGAGGA 950

QY 244 GCAGTCAACAGACGTAACGGGTGTGACGCTCTCAACGCTCTGACCAAGACTGGCT 303  
Db 951 GCAGTCAACAGACGTAACGGGTGTGACGCTCTCAACGCTCTGACCAAGACTGGCT 1010

QY 304 GAATGCAAGAGATCAAGTGAAGGTCTCCAAAGAGCCCTCCAGCCCTTCAGAA 363  
Db 1011 GAATGCAAGAGATCAAGTGAAGGTCTCCAAAGAGCCCTCCAGCCCTTCAGAA 1070

QY 364 AACCATCTCCAAAGCCAAAGGGGAGCCCGAGAAACCAAGGTGACACCTGCCCCATC 423  
Db 1071 AACCATCTCCAAAGCCAAAGGGGAGCCCGAGAAACCAAGGTGACACCTGCCCCATC 1130

QY 424 CCGGGATGAGCTACCAAGAACCAAGGTGACGCTCTGACCTGTGCAAAAGCTTATCC 483  
Db 1131 CCGGGATGAGCTACCAAGAACCAAGGTGACGCTCTGACCTGTGCAAAAGCTTATCC 1190

QY 484 CAGCGATCGCGGTGAGTGGAGAGCAATGGGCAAGCCGAGAAACAACTTACAAGCAC 543  
Db 1191 CAGCGATCGCGGTGAGTGGAGAGCAATGGGCAAGCCGAGAAACAACTTACAAGCAC 1250

QY 544 GCCTCCCGTGTGAGCTCGACGCGCTCTTCTTCTTACAGAGCTCACCGTGAACA 603  
Db 1251 GCCTCCCGTGTGAGCTCGACGCGCTCTTCTTCTTACAGAGCTCACCGTGAACA 1310

QY 604 GAGCAGTGGCAGCAGAGGAGAGCTTCTTCATGCTCCGTGATGATAGAGCTTGCACA 663  
Db 1311 GAGCAGTGGCAGCAGAGGAGAGAGCTTCTTCATGCTCCGTGATGATAGAGCTTGCACA 1370

QY 664 CCACTACAGCAGAGAGAGCTTCTTCTTCTCCGGG 639  
Db 1371 CCACTACAGCAGAGAGAGCTTCTTCTTCTCCGGG 1406

RESULT 13  
AX709548 1413 bp DNA linear PAT 04-APR-2003  
LOCUS Sequence 4 from Patent WO02096948.  
DEFINITION AX709548  
ACCESSION AX709548  
VERSION AX709548.1 GI:29564973  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE  
1 Braeslawsky, G.R., Hanna, N., Chinn, P. and Hariharan, K.  
AUTHORS Engineered retavalent antibodies and methods of use  
TITLE Patent: WO 02096948-A 4 05-DEC-2002;  
JOURNAL Idex Pharmaceuticals Corporation (US)  
FEATURES  
source 1..1413  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic nucleotide sequence of the C2B8 heavy chain"

ORIGIN

Query Match 90.4%; Score 694.4; DB 6; Length 1413;  
Best Local Similarity 99.9%; Pred. No. 2.3e-125;  
Matches 695; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 AGCAGAGCCCAATCTTGTGACAAACTCAACATGCCCGTCCAGACCTGAACT 63  
Db 711 AGCAGAGCCCAATCTTGTGACAAACTCAACATGCCCGTCCAGACCTGAACT 770

QY 64 CCGGGGGGAGCGTCAGTCTTCTTCCCGCCCAAAACCAAGAGACCTCATGATCTC 123  
Db 771 CCGGGGGGAGCGTCAGTCTTCTTCCCGCCCAAAACCAAGAGACCTCATGATCTC 830

QY 124 CCGGACCCCTGAGGTCAATGCTGTGTGACGTGAGCCAGAAACCTTGAGGTCA 183  
Db 831 CCGGACCCCTGAGGTCAATGCTGTGTGAGGTGAGCCAGAAACCTTGAGGTCA 890

QY 184 GTTCAACTGTGACGTGAGCGGCTGTGAGGTGATATGCAAGCAAAAGCCGGAGGA 243  
Db 891 GTTCAACTGTGACGTGAGCGGCTGTGAGGTGATATGCAAGCAAAAGCCGGAGGA 950

QY 244 GCAGTCAACAGACGTAACGGGTGTGACGCTCTCAACGCTCTGACCAAGACTGGCT 303  
Db 951 GCAGTCAACAGACGTAACGGGTGTGACGCTCTCAACGCTCTGACCAAGACTGGCT 1010

QY 304 GAATGCAAGAGATCAAGTGAAGGTCTCCAAAGAGCCCTCCAGCCCTTCAGAA 363  
Db 1011 GAATGCAAGAGATCAAGTGAAGGTCTCCAAAGAGCCCTCCAGCCCTTCAGAA 1070

QY 364 AACCATCTCCAAAGCCAAAGGGGAGCCCGAGAAACCAAGGTGACACCTGCCCCATC 423  
Db 1071 AACCATCTCCAAAGCCAAAGGGGAGCCCGAGAAACCAAGGTGACACCTGCCCCATC 1130

QY 424 CCGGGATGAGCTACCAAGAACCAAGGTGACGCTCTGACCTGTGCAAAAGCTTATCC 483  
Db 1131 CCGGGATGAGCTACCAAGAACCAAGGTGACGCTCTGACCTGTGCAAAAGCTTATCC 1190

QY 484 CAGCGATCGCGGTGAGTGGAGAGCAATGGGCAAGCCGAGAAACAACTTACAAGCAC 543  
Db 1191 CAGCGATCGCGGTGAGTGGAGAGCAATGGGCAAGCCGAGAAACAACTTACAAGCAC 1250

RESULT 14			
LOCUS	AR031186		
DEFINITION	AR031186	1428 bp	DNA
ACCESSION	AR031186		linear
VERSION	AR031186.1	GI:5945475	
KEYWORDS			
SOURCE	Unknown.		

```

JOURNAL Patent: US 5866125-A 19 02-FEB-1999;
FEATURES location/Qualifiers
Source 1. 1428
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

```

[illegible]

124 CCGAGCCCTGAGGTGACATGCGTGGTGGAGCTGAGCCGAGAACCTTGAGGTGCA 183  
786 CCTGGGGGAGACCGTCAATCTTCTCTTCCGCCAAACCAAGACACCTCTCATGATTC 845  
Ddb

846 CUGAACCCCGAGAGTCACATGCGTGGTGGACGTGAGCCACGAAAGCCCTTGAGGTCA 905  
184 GTTCAACTGTGATGCTGAGACGGCGTGGAGGTGCATATATCCCAAGCAAAAGCCGGCGAGGA 243  
906 GTTCACTGGTACTGATGACCGGGGTGAGAGGTGCATATATCCCAAGCAAAAGCCCTTGAGGTCA 965

244 GCAGTCAACAGACGCTACCGGGTGTGAGGTCCTCAACGGTCTGTGACACGAGACGGCT 303  
966 GCAGTCAACAGACGTCCTGGTGTGAGGTCCTCAACGGTCTGTGACACGAGACGGCT 1025  
304 GAATGCCAGAGCTCAAGTGTAGGTCCTCAACACCGCTGTGACACGAGACGGCT 1025

1026 GAATGCAAGCAGTGTCAAGTGCAGGCTCTCCAAATAAGCCCTTCCAGCCCCATCGAAGA 1085

424 CCGGGATGAGCTGACCAAGAAACAAGTCAAGCTGACCTGCTGCTCAAAAGCTTTATCC 483  
|||||  
1146 CCGGGAATGAGCTGACCAAGAAACAAGTCAAGCTGACCTGCTGCTCAAAAGCTTTATCC 1205  
|||||

RESULT 15			
AR042591			
LOCUS	AR042591	1428 bp	DNA
DEFINITION	Sequence	19	from patent US 5811524.
ACCESSION	AR042591		
VERSION	AR042591.1		
KEYWORDS	GI:5963087		
			linear
		PAT 29-SEP-1995	

SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
Unknown.	Unknown.	Unclassified.			
1 (bases 1 to 1429)			Brama, P., Charnat, S., Salim, P., L., Z., Walsh, E. E., Heard, C., Janne.	Neutralizing high affinity human monoclonal antibodies specific to RSV F-protein and methods for their manufacture and therapeutic use thereof	US 5,915,244-1, 10 23 Oct 1999

```
FEATURES
source      location/Qualifiers
            1..1428
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
```

	Query Match	90.4%;	Score 694.4;	DB 6;	Length 1428;
	Best Local Similarity	99.9%;	Pred. No. 2.3e-125;		
	Matches 695; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
OY	4 AGCAGAGCTTCAATTCCTTTGCGCATTAATTGGGTGAAC				

Db	.....CTCTGCAAAAGCACAATGCGACCGGCGCCAGACCTGAAT	63
726	AGCGAGCCCAATCTTGTGCAAAACCAACAATGCCACCGGTGGCACTTGAAT	785
Oy	.....CTCTGCAAAAGCACAATGCGACCGGCGCCAGACCTGAAT	63
64	CTGGGGGGGACCGTACGCTCTCTCTTCCCCCAAAACCAAGACAACCTATATATCTC	123

124 CGGACCCCTGAGTCACATGCGTGGTGGAGACGTGAGCCAGAGACCTGAGCTCAA 183  
846 CGGACCCCTGAGTCACATGCGTGGTGGAGACGTGAGCCAGAGACCTGAGCTCAA 805

[illegible][illegible]

364 AACCATCTCCAAAGGCCAAAGGCGACGCCCGAGAAACCAAGGTGTACACCTGTGCCCCATC 423  
 1086 AACCATCTCCAAAGGCCAAAGGCGACGCCCGAGAACCAAGGTGTACACCTGTGCCCCATC 1145



**This Page Blank (uspto)**